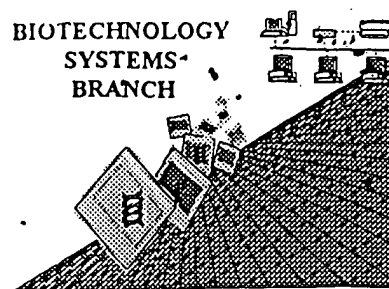# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/701926 A_

Source: _PCT09_

BEST AVAILABLE COPY

Date Processed by STIC: _11/14/01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _09/201926 A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P

1 ____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length.

Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ____ . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ____ Skipped Sequences
(OLD RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences
(NEW RULES)

Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequen
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10 ____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown is Artificial Sequence

11 ____ Use of <220>

Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represe any value not specifically a nucleotide.

AMC/MII – Biotechnology Systems Branch – 08/21/2001

PCT09

```
            RAW SEQUENCE LISTING              DATE: 11/14/2001
            PATENT APPLICATION:  US/09/701,926A    TIME: 13:53:41

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            Output Set: N:\CRF3\11142001\I701926A.raw

      3 <110> APPLICANT: THE UNIVERSITY OF QUEENSLAND
      5 <120> TITLE OF INVENTION: PHENOTYPE MODIFYING GENETIC SEQUENCES
      7 <130> FILE REFERENCE: 111590-120
      9 <140> CURRENT APPLICATION NUMBER: 09/701,926A
C--> 10 <141> CURRENT FILING DATE: 2000-12-04
     12 <150> PRIOR APPLICATION NUMBER: PP3901
     13 <151> PRIOR FILING DATE: 1998-06-04
     15 <150> PRIOR APPLICATION NUMBER: PP6174
     16 <151> PRIOR FILING DATE: 1988-09-25
     18 <150> PRIOR APPLICATION NUMBER: PP6169
     19 <151> PRIOR FILING DATE: 1998-09-25
     21 <150> PRIOR APPLICATION NUMBER: PP3903
     22 <151> PRIOR FILING DATE: 1998-06-04
     24 <160> NUMBER OF SEQ ID NOS: 39
     26 <170> SOFTWARE: PatentIn Ver. 2.0
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Handwritten: Does Not Comply Corrected Diskette Needed See pages 2, 4 and 8

Handwritten: Does Not Comply Corrected Diskette Needed

ERRORED SEQUENCES

Handwritten: Errored: Must Enumerate Unknown Example Field 221 "unsure" Field 222 (1...6263) Field 223 n = a or c or t or g

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     84 <212> TYPE: DNA
     85 <213> ORGANISM: Tomato
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     90 aacttcatca tcatacagta tggttttgat atgctcttcc attatcactg agccttatga 180
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     99 ttttcaaaat ccacctttgt tcaagcacta ccacgtcttt tcatctagcc cacaaccgtg 720
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Handwritten: ✗ The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors. ✗

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PATENT APPLICATION: US/09/701,926A   TIME: 13:53:41

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    325 <400> SEQUENCE: 12           sequences for similar errors.
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    330 gggatggtag ccccacggac aacgtaagat tcaggtaact tttatttata gtttcaactt 300
    331 gtgatgctga aattatagga attcgttaca tcagtgtaga ttccgaacac agtctgtgtg 360
    332 gtcttatgtg ttttgtaact tcttgcagca aaaggctaat gtgtttttata ctataaatac 420
    333 aagtcaagtt tgattgaacc acaaacaagg ctcattgtat ctgtatattg cacgcgaaag 480
```

```
      334 tggctagtgt atatagtatt gtcttatatc cgtcatcttg gaggaagaaa atcgtgtcct 540
      335 cagttttctg atattctgct catcaatcat cgactagcca atacactttg gccctacata 600
      336 tacacatact tatgagaagg aaaatacgaa atacgctcct tcaagacgag ttgaactttg 660
      337 taaattgttg tagtattagt atatgttaat gaggaaatgt agattttgtt gtagtttggt 720
      338 gatttgtaga atctgtctta taaagggact tacatgttga ggcaaactgt ataaaggtta 780
      339 aattgtcaat aacacacatc aaaatattgg accagtattt taagtaattt tttctgtata 840
      340 aaggctatgt tgctcaaatc cttcaaaaat ctcgacagat gcatggcacc ggtagtgcat 900
      341 tttttttgaat gagctggata cgagtgcaat aatatatttg ggaagtttga gcaaaataga 960
      342 cctgaaatta cttttagctt ttctttttta aaggaatcgg atatgggtac aataatattt 1020
      343 ttgaagagtc tgagcaacat agactactct cggtaggatg aggataagat tgaaatttta 1080
E--> 344 aaatgctcta aagagaaat ttgtggataa gattctccac taatttttnt atgacatgat 1140
      345 gagattctgc ctaagagttc caagaatatg gtgcacctgt taataatgta tatattataa 1200
      346 tagcataatc cactgttatg attttagcaa gctccttttt gtaatatatg aatgaacata 1260
      347 aatataaaaa aggagagtta tatttgaacc atataaaaaa tgttacaagt atttttatat 1320
      348 gaataatata ataaaaagta aacctttcg acaaaaaatt gattcatttc ccttttttaac 1380
      349 aattataacg gtttttaaat cctaatatac acctagtaaa aatatctatt tcaacccttc 1440
      350 tcgcagctgt attgcctaaa acccatatca cccccacgta gcctaaaatt tactttatac 1500
      351 tacgttgttt tgtttctcat ttttatttat ctttaattta tatcctgtaa aaagactcaa 1560
      352 agatgttttc tttaaatttt acttatttt ttttaggata aaaaatttgc aattcctaa  1619
      354 <210> SEQ ID NO: 13
      355 <211> LENGTH: 1193
      356 <212> TYPE: DNA
      357 <213> ORGANISM: Tomato
      359 <400> SEQUENCE: 13
      360 tgagtagaag ataaacttga caacgcatta gctcgaataa gagcataaat aaaaaagttt 60
      361 taactttaag aatccgtgca aaaaatcatc tactcaatta actcgatcaa tattctttca 120
      362 tcggtaactt acccgtttgg tattatatgt gtaaatatac ctaaatataa atacgagtct 180
      363 ataataacct aataaaaata ttaggcataa tagcggtgtt gttttgttag actcagtatt 240
      364 ttttatattt tataaaataa atactacgct ctttcaccaa acaattcttc aacgttaaat 300
      365 attcttgacg gtttttgttct gaaactatga ttctctttta gattttggtt ttgttgattt 360
      366 ctgatcaaaa actaaaagag aataattctt ctcccatttt attgctatct ttttatgatt 420
      367 gatttgttgg gggttcagca aatttattta tgttcttta gttttttcctc ttttatctgt 480
      368 atttgaatct tgatcaatta atgttctttg atcatttgtt tgttagaatc caaatacgcg 540
      369 agcaagagaa aaagatttag gaaatgagta aagattggat ttttatggga aagatctaaa 600
      370 gatttggttg aagggattaa tgaattgagc atatgagcta aaaaatcaat cttggtgagt 660
      371 agggtatgtt atttgtggaa gttttgttag cttttcttgt atgtattgat attagatgat 720
E--> 372 ttaaacagag tcactaacat tcatatagct gaccttgaat tgtttaggnc agtggcgtag 780
      373 tagttgttgt tgttataaga gaatgagtgc tatggggagg ataggtagtt acataggtag 840
E--> 374 aggggtacgt agtgtttcgg ggacgttgaa tccatttggt ggtnctgtgg atatcattgt 900
      375 ggtgaggcag ccagatggga gtttgaaatc aactccttgg tatgttagat ttgggaagat 960
      376 tcaggggtt ttgaaggcta gagaaaatgc ggttaatgta agtgtcaatg gcgttgaagc 1020
      377 tggttttcgt atgaatttag atactagagg gcaggcatac ttcctaaggg agcgagacat 1080
      378 ggaaaatgga tattctttaa ctactcgaac atttgaacaa cttgcacctt tgaatctgaa 1140
E--> 379 ggaggaaaga atgtggttga ttcncctgct caaaaccca gcccgggccg tcg         1193
      381 <210> SEQ ID NO: 14
      382 <211> LENGTH: 222
      383 <212> TYPE: DNA
      384 <213> ORGANISM: Tomato
      386 <400> SEQUENCE: 14
```

Field 222 (720..., 1193)

```
E--> 387 tatgttgctc aaatccttca aaaatctcga cagatgcatg nnnnnnnnng cacccggtag 60
     388 tgcatttttt tgaatgagct ggatacgagt gcaataatat atttgggaag tttgagcaaa 120
E--> 389 atagacctga aattactttt agcttttctt ttttaaagnn nnnnnnnnnn nngaatcgga 180
E--> 390 tatgggtaca ataatatttt tgaagagtcn tgagcaacat ag              222
     392 <210> SEQ ID NO: 15
     393 <211> LENGTH: 222
     394 <212> TYPE: DNA
     395 <213> ORGANISM: Potato
     397 <400> SEQUENCE: 15
     398 tatgttgctc aaacacttca aaaatgtcca caggtgcgtg tcggatactc caaaaagtag 60
E--> 399 tgtatttagg tgtgtgnnnn tgatattagt nnnagtgtat atttaggntg tgtgtggata 120
E--> 400 gtagnnntgt atttagatgt gtgtgatatt tcaaaaagtt gtgtattttg gagaatttga 180
     401 tacgggtgcg gcaacaattt tgaagagtca ggagcaaaat ag              222
     531 <210> SEQ ID NO: 32
     532 <211> LENGTH: 1588
     533 <212> TYPE: DNA
     534 <213> ORGANISM: Tomato
     536 <400> SEQUENCE: 32
     537 atcaagttga aatatgttaa caaaatgtac agttttatta tttttatttt atttataaaa 60
     538 aaaaaattgt acaaagaaac aaaatccctt ccttctgtat ttccatgtga tgtttaaatg 120
     539 gcatttgagt aaaagccaca aaaggcccat gtgaaattta taaaattttg aaacattttt 180
     540 gcataacaaa acaatacata agaggacacg taaaacttac taaaagagtt tttagttacg 240
     541 tataagcaaa gtttgagatt cccaagaaga aagagtttga aaatactaaa tgtcttgttg 300
     542 tcatccatat atatatatat gaatgaattc tcacatttgt gatcaagatt tctttatgca 360
E--> 543 tgntaatatt tatatttgga aattaaccgt cgattaatta agattatcat tgaataaggt 420
     544 ttgaaaaaga taaattgaac tatttcactt ttggagtgtt attgttatct gctaggtcaa 480
     545 tttagaatca taaattggaa ataaaaagac aacaatgccc ttttcttttc ttggatactt 540
     546 tgaggttgta ctaaaggaca tataaaaagg tgaaaaagct aaaagtttca ctaataacta 600
     547 attttattt tactttgtct tgtgtactaa acttttccat gtctttcct ttcaatttcc 660
     548 agttgtgatg gatagtaaat tttctatagc attcaacaca aggacaaaac actaagcaac 720
     549 aaaagcatcc aaaaaccaag attagcaatg tgcaaatgaa gctttatgta tgatcaaaaa 780
     550 cacaacttgg aagttggaac tacctatctt agattccatc acttttttt tgttctccat 840
     551 cgatattcat cgatattcag tattcgagct ccgattaaat cataattcga taaagcgtac 900
     552 tttaataaaa ataatttcac tcgaaggctt caatctgaaa ccactgatta ttaaaaatga 960
     553 aagaattcta tcattattcc atatctttt aggagattca agttaaaata gacaaccttt 1020
     554 ttctttaaat attgtcacaa tggtaataga tgcatgcgcg cctaatttca catttttaa 1080
     555 tataccaggc tatcattaac ttttttttta tttaaaaaac tttaatgatt tcgaagaaat 1140
     556 aatgactata taaaaaaaac aagaaatatt agtagccatc attatgtata tgagcaaaca 1200
     557 aaacgaaaat ggaactatgg caacatcatg gaagctagga ataaacagct ccacttcaca 1260
     558 agagaacaaa gttcatgttg tactattata ccttttttta ttttgacctc ttttaatatc 1320
     559 gtatatatta agcaagttgt taatcatata ccatctttta aatatttact tttgaaatca 1380
     560 taaaaaaatt gatgaaaaaa gttattatca tatctgttct tgcgtgagaa ataacaaata 1440
     561 tatttaagat gcacaaaaat tgattcgaac tagactttt ttaaaaaaaa ataaaaaaca 1500
     562 tgatgaaact ctaggtgggg tattctttt gtcaattact actaacaaag attgttgaaa 1560
     563 aagaagccaa ttatatgatt catcaata                             1588
     565 <210> SEQ ID NO: 33
     566 <211> LENGTH: 1307
     567 <212> TYPE: DNA
     568 <213> ORGANISM: Tomato
```

```
    570 <400> SEQUENCE: 33
    571 ttggacttcc tacccagcag ttcacacatc aatatcattt aattaaaatt aaagccattt 60
    572 atttaggaaa taaatagcat aaaaaaaaca ctaataatta aaacatttgt gtcaaaggga 120
    573 aagtatattg actaattttt tgcatatgtg gttcaaagga ggaatttttt aattacaaaa 180
    574 aaaaaagttt tatggtggga atcaaacata ttataggata attaaagaga tggatttatt 240
    575 atattttgtg taatctatta attattaaat ggcttaattt tgtatccact aataatataa 300
    576 gtaatttcta tatattcagt acaatttgac tagctccaac agctttccca gtaacacata 360
    577 tttatacagt tgcatctcac tataataaaa atatgtaaat attttctctt taccgtaact 420
    578 ccagtaaaac ttaaactcta attaataata caacactaat ctaggcaagc tgtagactgt 480
    579 aattaattgc atgtttttaaa tctgtgaagg gtcgtttggc ataaaaatac ataatgcagg 540
    580 gattattaac gtatagatta gtaatacata gattagtaat gcatggatta gttttttatca 600
    581 agtgtttgat tcattgtttc ctacttaatc ttatgtttag tttaaaactc tagaaaaata 660
    582 tatttcctat tataccttg agttattgtg agaatttgta tttcatttaa ctagtcaagt 720
E--> 583 taaatncnaa tttatatata tatatatata ttattaattt tgaggtgtga tatgtcacac 780
    584 tgtatatttt taattttttg ttggtcaaat ataccttgaa cttaaacatg gatttaaggc 840
E--> 585 tatttaaatt gttcaaatac acgaacctta ttttttttat aaaanaatca agtggtcaat 900
E--> 586 cgcaaactac atttataaaa naaaggccaa aaaaatcaat ccaatataac agctcataca 960
    587 tggagaaaaa attagtttat gaaatcatca aattacatgg aataaatttg gagaatttaa 1020
E--> 588 atgaatattt ataaatattt tcatataaat aaaaaagaac attaattaca aatanaataa 1080
    589 tagaaaaaaa atttgaggat attttagtca ttttggaatc ttttcgaagg attgctaaac 1140
    590 cttgaattag ctatccctcc atttcctagg gataaaataa gaccttgtat gaggtataac 1200
    591 taatctatgg attaggttaa ataaagtaac caaacaatat ttttgttgga ctaaattta 1260
E--> 592 atccatggat tcnttggatt aatacctcct accagcccgg gccgtcg            1307
    594 <210> SEQ ID NO: 34
    595 <211> LENGTH: 255
    596 <212> TYPE: DNA
    597 <213> ORGANISM: Tomato
    599 <400> SEQUENCE: 34
    600 ggtcgtttgg cataaaaata cataatgcag ggattattaa cgtatagatt agtaatacat 60
    601 agattagtaa tgcatggatt agtttttatc aagtgtttga ttcattgttt cctacttaat 120
E--> 602 cttatgttta gtttaaaact ctagaaaaat anntatttcc tattatacct ttgagttatt 180
E--> 603 gtgagaattt gtatttcatt taactnagtc aagttaaatn cnaatttata tatatata 240
    604 tatattatta atttt                                              255
    606 <210> SEQ ID NO: 35
    607 <211> LENGTH: 255
    608 <212> TYPE: DNA
    609 <213> ORGANISM: Tomato
    611 <400> SEQUENCE: 35
E--> 612 gatcgtacgg tacaaagatc aatacttcag gnnnnnnnnn nnnnnngagt agtaatacat 60
E-->·613 tttttggtaa tgcagagatt anttttatc aagtgtttgg ttcattgttt nttacctaat 120
    614 tttgtgtgtg gtttaaagtt tacaaaaaat aattctttcc aattatacgc taaagttatt 180
E--> 615 atgagatttt atatttcatg taattgggtc aannnaatag ataattgacc gataatatta 240
    616 ttttttataa cattt                                              255
    647 <210> SEQ ID NO: 39
    648 <211> LENGTH: 197
    649 <212> TYPE: DNA
    650 <213> ORGANISM: Tomato
    652 <400> SEQUENCE: 39
E--> 653 ttatatattt gtatttgtat aaagtgaaag agacgatgnn gagagtagcg agcgagatta 60
```

RAW SEQUENCE LISTING   DATE: 11/14/2001
PATENT APPLICATION: US/09/701,926A   TIME: 13:53:41

Input Set : **A:\sequencelisting.txt**
Output Set: **N:\CRF3\11142001\I701926A.raw**

E--> 654 aaaaagagtg gcgaacgnnn nnagatatgc cgtaaattag aattaaatga aactgtcatt 120
E--> 655 ataacattta ttttgaataa ataattttga tataatacac aattttcnnt taaaaagcaa 180
E--> 656 cgannnnnng ataatgt   197
E--> 659 - 1

Delete End of file Non ASCII text

VERIFICATION SUMMARY   DATE: 11/14/2001
PATENT APPLICATION: US/09/701,926A   TIME: 13:53:42

Input Set : **A:\sequencelisting.txt**
Output Set: **N:\CRF3\11142001\I701926A.raw**

```
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:136 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
M:340 Repeated in SeqNo=3
L:200 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
M:340 Repeated in SeqNo=4
L:285 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
L:314 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
L:326 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12
M:340 Repeated in SeqNo=12
L:372 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
M:340 Repeated in SeqNo=13
L:387 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
M:340 Repeated in SeqNo=14
L:399 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
M:340 Repeated in SeqNo=15
L:543 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:32
L:583 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:33
M:340 Repeated in SeqNo=33
L:602 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:34
M:340 Repeated in SeqNo=34
L:612 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:35
M:340 Repeated in SeqNo=35
L:653 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:39
M:340 Repeated in SeqNo=39
L:659 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:197 SEQ:39
```